

10/579662

IAP20 Rec'd PCT/PTO 17 MAY 2006

133-PCT1-US1.ST25.txt
SEQUENCE LISTING

<110> ELENA FEINSTEIN et al.

<120> DIAGNOSIS AND TREATMENT OF KIDNEY FIBROSIS AND OTHER FIBROTIC DISEASE

<130> 71541-A-PCT-US; 133/PCT1-US1

<140> Not Yet Known

<140> Herethwith

<150> 60/520,935

<151> 2003-11-17

<150> PCT/IL 2004/001049

<151> 2004-11-16

<160> 8

<170> PatentIn version 3.2

<210> 1

<211> 3225

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(3225)

<400> 1

atg tca ctg aaa aac gag cca cgg gta aat acc tct gca ctg cag aaa	48
Met Ser Leu Lys Asn Glu Pro Arg Val Asn Thr Ser Ala Leu Gln Lys	
1 5 10 15	
att gct gct gac atg agt aat atc ata gaa aat ctg gac acg cgg gaa	96
Ile Ala Ala Asp Met Ser Asn Ile Ile Glu Asn Leu Asp Thr Arg Glu	
20 25 30	
ctc cac ttt gag gga gag gag gta gac tac gac gtg tct ccc agc gat	144
Leu His Phe Glu Gly Glu Glu Val Asp Tyr Asp Val Ser Pro Ser Asp	
35 40 45	
ccc aag ata caa gaa gtg tat atc cct ttc tct gct att tat aac act	192
Pro Lys Ile Gln Glu Val Tyr Ile Pro Phe Ser Ala Ile Tyr Asn Thr	
50 55 60	
caa gga ttt aag gag cct aat ata cag acg tat ctc tcc ggc tgt cca	240
Gln Gly Phe Lys Glu Pro Asn Ile Gln Thr Tyr Leu Ser Gly Cys Pro	
65 70 75 80	
ata aaa gca caa gtt ctg gaa gtg gaa cgc ttc aca tct aca aca agg	288
Ile Lys Ala Gln Val Leu Glu Val Glu Arg Phe Thr Ser Thr Thr Arg	
85 90 95	
gta cca agt att aat ctt tac act att gaa tta aca cat ggg gaa ttt	336
Val Pro Ser Ile Asn Leu Tyr Thr Ile Glu Leu Thr His Gly Glu Phe	

133-PCT1-US1.ST25.txt

100	105	110	
aaa tgg caa gtt aag agg aaa ttc aag cat ttt caa gaa ttt cac aga Lys Trp Gln Val Lys Arg Lys Phe Lys His Phe Gln Glu Phe His Arg 115 120 125			384
gag ctg ctc aag tac aaa gcc ttt atc cgc atc ccc att ccc act aga Glu Leu Leu Lys Tyr Lys Ala Phe Ile Arg Ile Pro Ile Pro Thr Arg 130 135 140			432
aga cac acg ttt agg agg caa aac gtc aga gag gag cct cga gag atg Arg His Thr Phe Arg Arg Gln Asn Val Arg Glu Glu Pro Arg Glu Met 145 150 155 160			480
ccc agt ttg ccc cgt tca tct gaa aac atg ata aga gaa gaa caa ttc Pro Ser Leu Pro Arg Ser Ser Glu Asn Met Ile Arg Glu Glu Gln Phe 165 170 175			528
ctt ggt aga aga aaa caa ctg gaa gat tac ttg aca aag ata cta aaa Leu Gly Arg Arg Lys Gln Leu Glu Asp Tyr Leu Thr Lys Ile Leu Lys 180 185 190			576
atg ccc atg tat aga aac tat cat gcc aca aca gag ttt ctt gat ata Met Pro Met Tyr Arg Asn Tyr His Ala Thr Thr Glu Phe Leu Asp Ile 195 200 205			624
agc cag ctg tct ttc atc cat gat ttg gga cca aag ggc ata gaa ggt Ser Gln Leu Ser Phe Ile His Asp Leu Gly Pro Lys Gly Ile Glu Gly 210 215 220			672
atg ata atg aaa aga tct gga gga cac aga ata cca ggc ttg aat tgc Met Ile Met Lys Arg Ser Gly Gly His Arg Ile Pro Gly Leu Asn Cys 225 230 235 240			720
tgt ggt cag gga aga gcc tgc tac aga tgg tca aaa aga tgg tta ata Cys Gly Gln Gly Arg Ala Cys Tyr Arg Trp Ser Lys Arg Trp Leu Ile 245 250 255			768
gtg aaa gat tcc ttt tta ttg tat atg aaa cca gac agc ggt gcc att Val Lys Asp Ser Phe Leu Leu Tyr Met Lys Pro Asp Ser Gly Ala Ile 260 265 270			816
gcc ttc gtc ctg ctg gta gac aaa gaa ttc aaa att aag gtg ggg aag Ala Phe Val Leu Leu Val Asp Lys Glu Phe Lys Ile Lys Val Gly Lys 275 280 285			864
aag gag aca gaa acg aaa tat gga atc cga att gat aat ctt tca agg Lys Glu Thr Glu Thr Lys Tyr Gly Ile Arg Ile Asp Asn Leu Ser Arg 290 295 300			912
aca ctt att tta aaa tgc aac agc tat aga cat gct cgg tgg tgg gga Thr Leu Ile Leu Lys Cys Asn Ser Tyr Arg His Ala Arg Trp Trp Gly 305 310 315 320			960
ggg gct ata gaa gaa ttc atc cag aaa cat ggc acc aac ttt ctc aaa Gly Ala Ile Glu Glu Phe Ile Gln Lys His Gly Thr Asn Phe Leu Lys 325 330 335			1008
gat cat cga ttt ggg tca tat gct gct atc caa gag aat gct tta gct			1056

133-PCT1-US1.ST25.txt

Asp	His	Arg	Phe	Gly	Ser	Tyr	Ala	Ala	Ile	Gln	Glu	Asn	Ala	Leu	Ala		
			340					345					350				
aaa	tgg	tat	ggt	aat	gcc	aaa	gga	tat	ttt	gaa	gat	gtg	gca	aat	gca	1104	
Lys	Trp	Tyr	Val	Asn	Ala	Lys	Gly	Tyr	Phe	Glu	Asp	Val	Ala	Asn	Ala		
		355					360					365					
atg	gaa	gag	gca	aat	gaa	gag	att	ttt	atc	aca	gac	tgg	tgg	ctg	agt	1152	
Met	Glu	Glu	Ala	Asn	Glu	Glu	Ile	Phe	Ile	Thr	Asp	Trp	Trp	Leu	Ser		
	370					375					380						
cca	gaa	atc	ttc	ctg	aaa	cgc	cca	gtg	gtt	gag	gga	aat	cgt	tgg	agg	1200	
Pro	Glu	Ile	Phe	Leu	Lys	Arg	Pro	Val	Val	Glu	Gly	Asn	Arg	Trp	Arg		
385					390					395					400		
ttg	gac	tgc	att	ctt	aaa	cga	aaa	gca	caa	caa	gga	gtg	agg	atc	ttc	1248	
Leu	Asp	Cys	Ile	Leu	Lys	Arg	Lys	Ala	Gln	Gln	Gly	Val	Arg	Ile	Phe		
				405					410					415			
ata	atg	ctc	tac	aaa	gag	gtg	gaa	ctc	gct	ctt	ggc	atc	aat	agt	gaa	1296	
Ile	Met	Leu	Tyr	Lys	Glu	Val	Glu	Leu	Ala	Leu	Gly	Ile	Asn	Ser	Glu		
			420					425					430				
tac	acc	aag	agg	act	ttg	atg	cgt	cta	cat	ccc	aac	ata	aag	gtg	atg	1344	
Tyr	Thr	Lys	Arg	Thr	Leu	Met	Arg	Leu	His	Pro	Asn	Ile	Lys	Val	Met		
		435					440					445					
aga	cac	ccg	gat	cat	gtg	tca	tcc	acc	gtc	tat	ttg	tgg	gct	cac	cat	1392	
Arg	His	Pro	Asp	His	Val	Ser	Ser	Thr	Val	Tyr	Leu	Trp	Ala	His	His		
	450					455					460						
gag	aag	ctt	gtc	atc	att	gac	caa	tcg	gtg	gcc	ttt	gtg	gga	ggg	att	1440	
Glu	Lys	Leu	Val	Ile	Ile	Asp	Gln	Ser	Val	Ala	Phe	Val	Gly	Gly	Ile		
465					470					475					480		
gac	ctg	gcc	tat	gga	agg	tgg	gac	gac	aat	gag	cac	aga	ctc	aca	gac	1488	
Asp	Leu	Ala	Tyr	Gly	Arg	Trp	Asp	Asp	Asn	Glu	His	Arg	Leu	Thr	Asp		
				485					490					495			
gtg	ggc	agt	gtg	aag	cgg	gtc	act	tca	gga	ccg	tct	ctg	ggg	tcc	ctc	1536	
Val	Gly	Ser	Val	Lys	Arg	Val	Thr	Ser	Gly	Pro	Ser	Leu	Gly	Ser	Leu		
			500					505					510				
cca	cct	gcc	gca	atg	gag	tct	atg	gaa	tcc	tta	aga	ctc	aaa	gat	aaa	1584	
Pro	Pro	Ala	Ala	Met	Glu	Ser	Met	Glu	Ser	Leu	Arg	Leu	Lys	Asp	Lys		
		515					520					525					
aat	gag	cct	gtt	caa	aac	cta	ccc	atc	cag	aag	agt	att	gat	gat	gtg	1632	
Asn	Glu	Pro	Val	Gln	Asn	Leu	Pro	Ile	Gln	Lys	Ser	Ile	Asp	Asp	Val		
	530					535					540						
gat	tca	aaa	ctg	aaa	gga	ata	gga	aag	cca	aga	aag	ttc	tcc	aaa	ttt	1680	
Asp	Ser	Lys	Leu	Lys	Gly	Ile	Gly	Lys	Pro	Arg	Lys	Phe	Ser	Lys	Phe		
545					550				555						560		
agt	ctc	tac	aag	cag	ctc	cac	agg	cac	cac	ctg	cac	gac	gca	gat	agc	1728	
Ser	Leu	Tyr	Lys	Gln	Leu	His	Arg	His	His	Leu	His	Asp	Ala	Asp	Ser		
				565					570					575			

133-PCT1-US1.ST25.txt

atc agc agc att gac agc acc tcc agt tat ttt aat cac tat aga agt Ile Ser Ser Ile Asp Ser Thr Ser Ser Tyr Phe Asn His Tyr Arg Ser 580 585 590	1776
cat cac aat tta atc cat ggt tta aaa ccc cac ttc aaa ctc ttt cac His His Asn Leu Ile His Gly Leu Lys Pro His Phe Lys Leu Phe His 595 600 605	1824
ccg tcc agt gag tct gag caa gga ctc act aga cct cat gct gat acc Pro Ser Ser Glu Ser Glu Gln Gly Leu Thr Arg Pro His Ala Asp Thr 610 615 620	1872
ggg tcc atc cgt agt tta cag aca ggt gtg gga gag ctg cat ggg gaa Gly Ser Ile Arg Ser Leu Gln Thr Gly Val Gly Glu Leu His Gly Glu 625 630 635 640	1920
acc aga ttc tgg cat gga aag gac tac tgc aat ttc gtc ttc aaa gac Thr Arg Phe Trp His Gly Lys Asp Tyr Cys Asn Phe Val Phe Lys Asp 645 650 655	1968
tgg gtt caa ctt gat aaa cct ttt gct gat ttc att gac agg tac tcc Trp Val Gln Leu Asp Lys Pro Phe Ala Asp Phe Ile Asp Arg Tyr Ser 660 665 670	2016
acg ccc cgg atg ccc tgg cat gac att gcc tct gca gtc cac ggg aag Thr Pro Arg Met Pro Trp His Asp Ile Ala Ser Ala Val His Gly Lys 675 680 685	2064
gcg gct cgt gat gtg gca cgt cac ttc atc cag cgc tgg aac ttc aca Ala Ala Arg Asp Val Ala Arg His Phe Ile Gln Arg Trp Asn Phe Thr 690 695 700	2112
aaa att atg aaa tca aaa tat cgg tcc ctt tct tat cct ttt ctg ctt Lys Ile Met Lys Ser Lys Tyr Arg Ser Leu Ser Tyr Pro Phe Leu Leu 705 710 715 720	2160
cca aag tct caa aca aca gcc cat gag ttg aga tat caa gtg cct ggg Pro Lys Ser Gln Thr Thr Ala His Glu Leu Arg Tyr Gln Val Pro Gly 725 730 735	2208
tct gtc cat gct aac gta cag ttg ctc cgc tct gct gct gat tgg tct Ser Val His Ala Asn Val Gln Leu Leu Arg Ser Ala Ala Asp Trp Ser 740 745 750	2256
gct ggt ata aag tac cat gaa gag tcc atc cac gcc gct tac gtc cat Ala Gly Ile Lys Tyr His Glu Glu Ser Ile His Ala Ala Tyr Val His 755 760 765	2304
gtg ata gag aac agc agg cac tat atc tat atc gaa aac cag ttt ttc Val Ile Glu Asn Ser Arg His Tyr Ile Tyr Ile Glu Asn Gln Phe Phe 770 775 780	2352
ata agc tgt gct gat gac aaa gtt gtg ttc aac aag ata ggc gat gcc Ile Ser Cys Ala Asp Asp Lys Val Val Phe Asn Lys Ile Gly Asp Ala 785 790 795 800	2400
att gcc cag agg atc ctg aaa gct cac agg gaa aac cag aaa tac cgg Ile Ala Gln Arg Ile Leu Lys Ala His Arg Glu Asn Gln Lys Tyr Arg 805 810 815	2448

133-PCT1-US1.ST25.txt

gta tat gtc gtg ata cca ctt ctg cca ggg ttc gaa gga gac att tca	2496
Val Tyr Val Val Ile Pro Leu Leu Pro Gly Phe Glu Gly Asp Ile Ser	
820 825 830	
acc ggc gga gga aat gct cta cag gca atc atg cac ttc aac tac aga	2544
Thr Gly Gly Gly Asn Ala Leu Gln Ala Ile Met His Phe Asn Tyr Arg	
835 840 845	
acc atg tgc aga gga gaa aat tcc atc ctt gga cag tta aaa gca gag	2592
Thr Met Cys Arg Gly Glu Asn Ser Ile Leu Gly Gln Leu Lys Ala Glu	
850 855 860	
ctt ggt aat cag tgg ata aat tac ata tca ttc tgt ggt ctt aga aca	2640
Leu Gly Asn Gln Trp Ile Asn Tyr Ile Ser Phe Cys Gly Leu Arg Thr	
865 870 875 880	
cat gca gag ctc gaa gga aac cta gta act gag ctt atc tat gtc cac	2688
His Ala Glu Leu Glu Gly Asn Leu Val Thr Glu Leu Ile Tyr Val His	
885 890 895	
agc aag ttg tta att gct gat gat aac act gtt att att ggc tct gcc	2736
Ser Lys Leu Leu Ile Ala Asp Asp Asn Thr Val Ile Ile Gly Ser Ala	
900 905 910	
aac ata aat gac cgc agc atg ctg gga aag cgt gac agt gaa atg gct	2784
Asn Ile Asn Asp Arg Ser Met Leu Gly Lys Arg Asp Ser Glu Met Ala	
915 920 925	
gtc att gtg caa gat aca gag act gtt cct tca gta atg gat gga aaa	2832
Val Ile Val Gln Asp Thr Glu Thr Val Pro Ser Val Met Asp Gly Lys	
930 935 940	
gag tac caa gct ggc cgg ttt gcc cga gga ctt cgg cta cag tgc ttt	2880
Glu Tyr Gln Ala Gly Arg Phe Ala Arg Gly Leu Arg Leu Gln Cys Phe	
945 950 955 960	
agg gtt gtc ctt ggc tat ctt gat gac cca agt gag gac att cag gat	2928
Arg Val Val Leu Gly Tyr Leu Asp Asp Pro Ser Glu Asp Ile Gln Asp	
965 970 975	
cca gtg agt gac aaa ttc ttc aag gag gtg tgg gtt tca aca gca gct	2976
Pro Val Ser Asp Lys Phe Phe Lys Glu Val Trp Val Ser Thr Ala Ala	
980 985 990	
cga aat gct aca att tat gac aag gtt ttc cgg tgc ctt ccc aat gat	3024
Arg Asn Ala Thr Ile Tyr Asp Lys Val Phe Arg Cys Leu Pro Asn Asp	
995 1000 1005	
gaa gta cac aat tta att cag ctg aga gac ttt ata aac aag ccc	3069
Glu Val His Asn Leu Ile Gln Leu Arg Asp Phe Ile Asn Lys Pro	
1010 1015 1020	
gta tta gct aag gaa gat ccc att cga gct gag gag gaa ctg aag	3114
Val Leu Ala Lys Glu Asp Pro Ile Arg Ala Glu Glu Glu Leu Lys	
1025 1030 1035	
aag atc cgt gga ttt ttg gtg caa ttc ccc ttt tat ttc ttg tct	3159
Lys Ile Arg Gly Phe Leu Val Gln Phe Pro Phe Tyr Phe Leu Ser	

133-PCT1-US1.ST25.txt

1040

1045

1050

gaa gaa agc cta ctg cct tct gtt ggg acc aaa gag gcc ata gtg 3204
 Glu Glu Ser Leu Leu Pro Ser Val Gly Thr Lys Glu Ala Ile Val
 1055 1060 1065

ccc atg gag gtt tgg act taa 3225
 Pro Met Glu Val Trp Thr
 1070

<210> 2
 <211> 1074
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Ser Leu Lys Asn Glu Pro Arg Val Asn Thr Ser Ala Leu Gln Lys
 1 5 10 15

Ile Ala Ala Asp Met Ser Asn Ile Ile Glu Asn Leu Asp Thr Arg Glu
 20 25 30

Leu His Phe Glu Gly Glu Glu Val Asp Tyr Asp Val Ser Pro Ser Asp
 35 40 45

Pro Lys Ile Gln Glu Val Tyr Ile Pro Phe Ser Ala Ile Tyr Asn Thr
 50 55 60

Gln Gly Phe Lys Glu Pro Asn Ile Gln Thr Tyr Leu Ser Gly Cys Pro
 65 70 75 80

Ile Lys Ala Gln Val Leu Glu Val Glu Arg Phe Thr Ser Thr Thr Arg
 85 90 95

Val Pro Ser Ile Asn Leu Tyr Thr Ile Glu Leu Thr His Gly Glu Phe
 100 105 110

Lys Trp Gln Val Lys Arg Lys Phe Lys His Phe Gln Glu Phe His Arg
 115 120 125

Glu Leu Leu Lys Tyr Lys Ala Phe Ile Arg Ile Pro Ile Pro Thr Arg
 130 135 140

Arg His Thr Phe Arg Arg Gln Asn Val Arg Glu Glu Pro Arg Glu Met
 145 150 155 160

Pro Ser Leu Pro Arg Ser Ser Glu Asn Met Ile Arg Glu Glu Gln Phe

133-PCT1-US1.ST25.txt

165

170

175

Leu Gly Arg Arg Lys Gln Leu Glu Asp Tyr Leu Thr Lys Ile Leu Lys
 180 185 190

Met Pro Met Tyr Arg Asn Tyr His Ala Thr Thr Glu Phe Leu Asp Ile
 195 200 205

Ser Gln Leu Ser Phe Ile His Asp Leu Gly Pro Lys Gly Ile Glu Gly
 210 215 220

Met Ile Met Lys Arg Ser Gly Gly His Arg Ile Pro Gly Leu Asn Cys
 225 230 235 240

Cys Gly Gln Gly Arg Ala Cys Tyr Arg Trp Ser Lys Arg Trp Leu Ile
 245 250 255

Val Lys Asp Ser Phe Leu Leu Tyr Met Lys Pro Asp Ser Gly Ala Ile
 260 265 270

Ala Phe Val Leu Leu Val Asp Lys Glu Phe Lys Ile Lys Val Gly Lys
 275 280 285

Lys Glu Thr Glu Thr Lys Tyr Gly Ile Arg Ile Asp Asn Leu Ser Arg
 290 295 300

Thr Leu Ile Leu Lys Cys Asn Ser Tyr Arg His Ala Arg Trp Trp Gly
 305 310 315 320

Gly Ala Ile Glu Glu Phe Ile Gln Lys His Gly Thr Asn Phe Leu Lys
 325 330 335

Asp His Arg Phe Gly Ser Tyr Ala Ala Ile Gln Glu Asn Ala Leu Ala
 340 345 350

Lys Trp Tyr Val Asn Ala Lys Gly Tyr Phe Glu Asp Val Ala Asn Ala
 355 360 365

Met Glu Glu Ala Asn Glu Glu Ile Phe Ile Thr Asp Trp Trp Leu Ser
 370 375 380

Pro Glu Ile Phe Leu Lys Arg Pro Val Val Glu Gly Asn Arg Trp Arg
 385 390 395 400

133-PCT1-US1.ST25.txt

Leu Asp Cys Ile Leu Lys Arg Lys Ala Gln Gln Gly Val Arg Ile Phe
 405 410 415
 Ile Met Leu Tyr Lys Glu Val Glu Leu Ala Leu Gly Ile Asn Ser Glu
 420 425 430
 Tyr Thr Lys Arg Thr Leu Met Arg Leu His Pro Asn Ile Lys Val Met
 435 440 445
 Arg His Pro Asp His Val Ser Ser Thr Val Tyr Leu Trp Ala His His
 450 455 460
 Glu Lys Leu Val Ile Ile Asp Gln Ser Val Ala Phe Val Gly Gly Ile
 465 470 475 480
 Asp Leu Ala Tyr Gly Arg Trp Asp Asp Asn Glu His Arg Leu Thr Asp
 485 490 495
 Val Gly Ser Val Lys Arg Val Thr Ser Gly Pro Ser Leu Gly Ser Leu
 500 505 510
 Pro Pro Ala Ala Met Glu Ser Met Glu Ser Leu Arg Leu Lys Asp Lys
 515 520 525
 Asn Glu Pro Val Gln Asn Leu Pro Ile Gln Lys Ser Ile Asp Asp Val
 530 535 540
 Asp Ser Lys Leu Lys Gly Ile Gly Lys Pro Arg Lys Phe Ser Lys Phe
 545 550 555 560
 Ser Leu Tyr Lys Gln Leu His Arg His His Leu His Asp Ala Asp Ser
 565 570 575
 Ile Ser Ser Ile Asp Ser Thr Ser Ser Tyr Phe Asn His Tyr Arg Ser
 580 585 590
 His His Asn Leu Ile His Gly Leu Lys Pro His Phe Lys Leu Phe His
 595 600 605
 Pro Ser Ser Glu Ser Glu Gln Gly Leu Thr Arg Pro His Ala Asp Thr
 610 615 620
 Gly Ser Ile Arg Ser Leu Gln Thr Gly Val Gly Glu Leu His Gly Glu
 625 630 635 640

133-PCT1-US1.ST25.txt

Thr Arg Phe Trp His Gly Lys Asp Tyr Cys Asn Phe Val Phe Lys Asp
645 650 655

Trp Val Gln Leu Asp Lys Pro Phe Ala Asp Phe Ile Asp Arg Tyr Ser
660 665 670

Thr Pro Arg Met Pro Trp His Asp Ile Ala Ser Ala Val His Gly Lys
675 680 685

Ala Ala Arg Asp Val Ala Arg His Phe Ile Gln Arg Trp Asn Phe Thr
690 695 700

Lys Ile Met Lys Ser Lys Tyr Arg Ser Leu Ser Tyr Pro Phe Leu Leu
705 710 715 720

Pro Lys Ser Gln Thr Thr Ala His Glu Leu Arg Tyr Gln Val Pro Gly
725 730 735

Ser Val His Ala Asn Val Gln Leu Leu Arg Ser Ala Ala Asp Trp Ser
740 745 750

Ala Gly Ile Lys Tyr His Glu Glu Ser Ile His Ala Ala Tyr Val His
755 760 765

Val Ile Glu Asn Ser Arg His Tyr Ile Tyr Ile Glu Asn Gln Phe Phe
770 775 780

Ile Ser Cys Ala Asp Asp Lys Val Val Phe Asn Lys Ile Gly Asp Ala
785 790 795 800

Ile Ala Gln Arg Ile Leu Lys Ala His Arg Glu Asn Gln Lys Tyr Arg
805 810 815

Val Tyr Val Val Ile Pro Leu Leu Pro Gly Phe Glu Gly Asp Ile Ser
820 825 830

Thr Gly Gly Gly Asn Ala Leu Gln Ala Ile Met His Phe Asn Tyr Arg
835 840 845

Thr Met Cys Arg Gly Glu Asn Ser Ile Leu Gly Gln Leu Lys Ala Glu
850 855 860

Leu Gly Asn Gln Trp Ile Asn Tyr Ile Ser Phe Cys Gly Leu Arg Thr
865 870 875 880

133-PCT1-US1.ST25.txt

His Ala Glu Leu Glu Gly Asn Leu Val Thr Glu Leu Ile Tyr Val His
885 890 895

Ser Lys Leu Leu Ile Ala Asp Asp Asn Thr Val Ile Ile Gly Ser Ala
900 905 910

Asn Ile Asn Asp Arg Ser Met Leu Gly Lys Arg Asp Ser Glu Met Ala
915 920 925

Val Ile Val Gln Asp Thr Glu Thr Val Pro Ser Val Met Asp Gly Lys
930 935 940

Glu Tyr Gln Ala Gly Arg Phe Ala Arg Gly Leu Arg Leu Gln Cys Phe
945 950 955 960

Arg Val Val Leu Gly Tyr Leu Asp Asp Pro Ser Glu Asp Ile Gln Asp
965 970 975

Pro Val Ser Asp Lys Phe Phe Lys Glu Val Trp Val Ser Thr Ala Ala
980 985 990

Arg Asn Ala Thr Ile Tyr Asp Lys Val Phe Arg Cys Leu Pro Asn Asp
995 1000 1005

Glu Val His Asn Leu Ile Gln Leu Arg Asp Phe Ile Asn Lys Pro
1010 1015 1020

Val Leu Ala Lys Glu Asp Pro Ile Arg Ala Glu Glu Glu Leu Lys
1025 1030 1035

Lys Ile Arg Gly Phe Leu Val Gln Phe Pro Phe Tyr Phe Leu Ser
1040 1045 1050

Glu Glu Ser Leu Leu Pro Ser Val Gly Thr Lys Glu Ala Ile Val
1055 1060 1065

Pro Met Glu Val Trp Thr
1070

<210> 3
<211> 2802
<212> DNA
<213> Homo sapiens

133-PCT1-US1.ST25.txt

<220>

<221> CDS

<222> (1)..(2802)

<400> 3

atg acg gcg acc cct gag agc ctc ttc ccc act ggg gac gaa ctg gac	48
Met Thr Ala Thr Pro Glu Ser Leu Phe Pro Thr Gly Asp Glu Leu Asp	
1 5 10 15	
tcc agc cag ctg cag atg gag tcc gat gag gtg gac acc ctg aag gag	96
Ser Ser Gln Leu Gln Met Glu Ser Asp Glu Val Asp Thr Leu Lys Glu	
20 25 30	
gga gag gac cca gcc gac cgg atg cac ccg ttt ctg gcc atc tat gag	144
Gly Glu Asp Pro Ala Asp Arg Met His Pro Phe Leu Ala Ile Tyr Glu	
35 40 45	
ctt cag tct ctg aaa gtg cac ccc ttg gtg ttc gca cct ggg gtc cct	192
Leu Gln Ser Leu Lys Val His Pro Leu Val Phe Ala Pro Gly Val Pro	
50 55 60	
gtc aca gcc cag gtg gtg ggc acc gaa aga tat acc agc gga tcc aag	240
Val Thr Ala Gln Val Val Gly Thr Glu Arg Tyr Thr Ser Gly Ser Lys	
65 70 75 80	
gtg gga acc tgc act ctg tat tct gtc cgc ttg act cac ggc gac ttt	288
Val Gly Thr Cys Thr Leu Tyr Ser Val Arg Leu Thr His Gly Asp Phe	
85 90 95	
tcc tgg aca acc aag aag aaa tac cgt cat ttt cag gag ctg cat cgg	336
Ser Trp Thr Thr Lys Lys Lys Tyr Arg His Phe Gln Glu Leu His Arg	
100 105 110	
gac ctc ctg aga cac aaa gtc ttg atg agt ctg ctc cct ctg gct cga	384
Asp Leu Leu Arg His Lys Val Leu Met Ser Leu Leu Pro Leu Ala Arg	
115 120 125	
ttt gcc gtt gcc tat tct cca gcc cga gat gca ggc aac aga gag atg	432
Phe Ala Val Ala Tyr Ser Pro Ala Arg Asp Ala Gly Asn Arg Glu Met	
130 135 140	
ccc tct cta ccc cgg gca ggt cct gag ggc tcc acc aga cat gca gcc	480
Pro Ser Leu Pro Arg Ala Gly Pro Glu Gly Ser Thr Arg His Ala Ala	
145 150 155 160	
agc aaa cag aaa tac ctg gag aat tac ctc aac tgt ctc ttg acc atg	528
Ser Lys Gln Lys Tyr Leu Glu Asn Tyr Leu Asn Cys Leu Leu Thr Met	
165 170 175	
tct ttc tat cgc aac tac cat gcc atg aca gag ttc ctg gaa gtc agt	576
Ser Phe Tyr Arg Asn Tyr His Ala Met Thr Glu Phe Leu Glu Val Ser	
180 185 190	
cag ctg tcc ttt atc ccg gac ttg ggc cgc aaa gga ctg gag ggg atg	624
Gln Leu Ser Phe Ile Pro Asp Leu Gly Arg Lys Gly Leu Glu Gly Met	
195 200 205	
atc cgg aag cgc tca ggt ggc cac cgt gtt cct ggc ctc acc tgc tgt	672

133-PCT1-US1.ST25.txt

Ile	Arg	Lys	Arg	Ser	Gly	Gly	His	Arg	Val	Pro	Gly	Leu	Thr	Cys	Cys		
210						215					220						
ggc	cga	gac	caa	gtt	tgt	tat	cgc	tgg	tcc	aag	agg	tgg	ctg	gtg	gtg	720	
Gly	Arg	Asp	Gln	Val	Cys	Tyr	Arg	Trp	Ser	Lys	Arg	Trp	Leu	Val	Val		240
225					230					235							
aag	gac	tcc	ttc	ctg	ctg	tac	atg	tgc	ctc	gag	aca	ggg	gcc	atc	tca	768	
Lys	Asp	Ser	Phe	Leu	Leu	Tyr	Met	Cys	Leu	Glu	Thr	Gly	Ala	Ile	Ser		255
				245					250					255			
ttt	gtt	cag	ctc	ttt	gac	cct	ggc	ttt	gag	gtg	caa	gtg	ggg	aaa	agg	816	
Phe	Val	Gln	Leu	Phe	Asp	Pro	Gly	Phe	Glu	Val	Gln	Val	Gly	Lys	Arg		270
			260					265									
agc	acg	gag	gca	cgg	cac	ggc	gtg	cgg	atc	gat	acc	tcc	cac	agg	tcc	864	
Ser	Thr	Glu	Ala	Arg	His	Gly	Val	Arg	Ile	Asp	Thr	Ser	His	Arg	Ser		285
		275					280					285					
ttg	att	ctc	aag	tgc	agc	agc	tac	cgg	cag	gca	cgg	tgg	tgg	gcc	caa	912	
Leu	Ile	Leu	Lys	Cys	Ser	Ser	Tyr	Arg	Gln	Ala	Arg	Trp	Trp	Ala	Gln		300
	290					295					300						
gag	atc	act	gag	ctg	gca	cag	ggc	cca	ggc	aga	gac	ttc	cta	cag	ctg	960	
Glu	Ile	Thr	Glu	Leu	Ala	Gln	Gly	Pro	Gly	Arg	Asp	Phe	Leu	Gln	Leu		320
305					310					315							
cac	cgg	cat	gac	agc	tac	gcc	cca	ccc	cgg	cct	ggg	acc	ttg	gcc	cgg	1008	
His	Arg	His	Asp	Ser	Tyr	Ala	Pro	Pro	Arg	Pro	Gly	Thr	Leu	Ala	Arg		335
				325					330					335			
tgg	ttt	gtg	aat	ggg	gca	ggt	tac	ttt	gct	gct	gtg	gca	gat	gcc	atc	1056	
Trp	Phe	Val	Asn	Gly	Ala	Gly	Tyr	Phe	Ala	Ala	Val	Ala	Asp	Ala	Ile		350
			340					345						350			
ctt	cga	gct	caa	gag	gag	att	ttc	atc	aca	gac	tgg	tgg	ttg	agt	cct	1104	
Leu	Arg	Ala	Gln	Glu	Glu	Ile	Phe	Ile	Thr	Asp	Trp	Trp	Leu	Ser	Pro		365
		355					360										
gag	gtt	tac	ctg	aag	cgt	ccg	gcc	cat	tca	gat	gac	tgg	aga	ctg	gac	1152	
Glu	Val	Tyr	Leu	Lys	Arg	Pro	Ala	His	Ser	Asp	Asp	Trp	Arg	Leu	Asp		380
	370					375					380						
att	atg	ctc	aag	agg	aag	gcg	gag	gaa	ggt	gtc	cgt	gtg	tct	att	ctg	1200	
Ile	Met	Leu	Lys	Arg	Lys	Ala	Glu	Glu	Gly	Val	Arg	Val	Ser	Ile	Leu		400
385					390					395							
ctg	ttt	aaa	gaa	gtg	gaa	ttg	gcc	ttg	ggc	atc	aac	agt	ggc	tat	agc	1248	
Leu	Phe	Lys	Glu	Val	Glu	Leu	Ala	Leu	Gly	Ile	Asn	Ser	Gly	Tyr	Ser		415
				405					410					415			
aag	agg	gcg	ctg	atg	ctg	ctg	cac	ccc	aac	ata	aag	gtg	atg	cgt	cac	1296	
Lys	Arg	Ala	Leu	Met	Leu	Leu	His	Pro	Asn	Ile	Lys	Val	Met	Arg	His		430
			420					425									
cca	gac	caa	gtg	acg	ttg	tgg	gcc	cat	cat	gag	aag	ctc	ctg	gtg	gtg	1344	
Pro	Asp	Gln	Val	Thr	Leu	Trp	Ala	His	His	Glu	Lys	Leu	Leu	Val	Val		445
		435					440					445					

133-PCT1-US1.ST25.txt

gac	caa	gtg	gta	gca	ttc	ctg	ggg	gga	ctg	gac	ctt	gcc	tat	ggc	cgc	1392
Asp	Gln	Val	Val	Ala	Phe	Leu	Gly	Gly	Leu	Asp	Leu	Ala	Tyr	Gly	Arg	
	450					455					460					
tgg	gat	gac	ctg	cac	tac	cga	ctg	act	gac	ctt	gga	gac	tcc	tct	gaa	1440
Trp	Asp	Asp	Leu	His	Tyr	Arg	Leu	Thr	Asp	Leu	Gly	Asp	Ser	Ser	Glu	
465					470					475					480	
tca	gct	gcc	tcc	cag	cct	ccc	acc	ccg	cgc	cca	gac	tca	cca	gcc	acc	1488
Ser	Ala	Ala	Ser	Gln	Pro	Pro	Thr	Pro	Arg	Pro	Asp	Ser	Pro	Ala	Thr	
				485					490					495		
cca	gac	ctc	tct	cac	aac	caa	ttc	ttc	tgg	ctg	ggc	aag	gac	tac	agc	1536
Pro	Asp	Leu	Ser	His	Asn	Gln	Phe	Phe	Trp	Leu	Gly	Lys	Asp	Tyr	Ser	
			500					505					510			
aat	ctt	atc	acc	aag	gac	tgg	gtg	cag	ctg	gac	cgg	cct	ttc	gaa	gat	1584
Asn	Leu	Ile	Thr	Lys	Asp	Trp	Val	Gln	Leu	Asp	Arg	Pro	Phe	Glu	Asp	
		515					520					525				
ttc	att	gac	agg	gag	acg	acc	cct	cgg	atg	cca	tgg	cgg	gac	gtt	ggg	1632
Phe	Ile	Asp	Arg	Glu	Thr	Thr	Pro	Arg	Met	Pro	Trp	Arg	Asp	Val	Gly	
	530					535					540					
gtg	gtc	gtc	cat	ggc	cta	ccg	gcc	cgg	gac	ctt	gcc	cgg	cac	ttc	atc	1680
Val	Val	Val	His	Gly	Leu	Pro	Ala	Arg	Asp	Leu	Ala	Arg	His	Phe	Ile	
545					550					555					560	
cag	cgc	tgg	aac	ttc	acc	aag	acc	acc	aag	gcc	aag	tac	aag	act	ccc	1728
Gln	Arg	Trp	Asn	Phe	Thr	Lys	Thr	Thr	Lys	Ala	Lys	Tyr	Lys	Thr	Pro	
				565					570					575		
ata	tac	ccc	tac	ctg	ctt	ccc	aag	tct	acc	agc	acg	gcc	aat	cag	ctc	1776
Ile	Tyr	Pro	Tyr	Leu	Leu	Pro	Lys	Ser	Thr	Ser	Thr	Ala	Asn	Gln	Leu	
			580					585					590			
ccc	ttc	aca	ctt	cca	gga	ggg	cag	tgc	acc	acc	gta	cag	gtc	ttg	cga	1824
Pro	Phe	Thr	Leu	Pro	Gly	Gly	Gln	Cys	Thr	Thr	Val	Gln	Val	Leu	Arg	
		595					600					605				
tca	gtg	gac	cgc	tgg	tca	gca	ggg	act	ctg	gag	aac	tcc	atc	ctc	aat	1872
Ser	Val	Asp	Arg	Trp	Ser	Ala	Gly	Thr	Leu	Glu	Asn	Ser	Ile	Leu	Asn	
	610					615					620					
gcc	tac	ctg	cac	acc	atc	agg	gag	agc	cag	cac	ttc	ctc	tac	att	gag	1920
Ala	Tyr	Leu	His	Thr	Ile	Arg	Glu	Ser	Gln	His	Phe	Leu	Tyr	Ile	Glu	
625					630					635					640	
aat	cag	ttc	ttc	att	agc	tgc	tca	gat	ggg	cgg	acg	gtt	ctg	aac	aag	1968
Asn	Gln	Phe	Phe	Ile	Ser	Cys	Ser	Asp	Gly	Arg	Thr	Val	Leu	Asn	Lys	
				645					650					655		
gtg	ggc	gat	gag	att	gtg	gac	aga	atc	ctg	aag	gcc	cac	aaa	cag	ggg	2016
Val	Gly	Asp	Glu	Ile	Val	Asp	Arg	Ile	Leu	Lys	Ala	His	Lys	Gln	Gly	
			660					665					670			
tgg	tgt	tac	cga	gtc	tac	gtg	ctt	ttg	ccc	tta	ctc	cct	ggc	ttc	gag	2064
Trp	Cys	Tyr	Arg	Val	Tyr	Val	Leu	Leu	Pro	Leu	Leu	Pro	Gly	Phe	Glu	
		675					680					685				

133-PCT1-US1.ST25.txt

ggt gac atc tcc acg ggc ggt ggc aac tcc atc cag gcc att ctg cac Gly Asp Ile Ser Thr Gly Gly Gly Asn Ser Ile Gln Ala Ile Leu His 690 695 700	2112
ttt act tac agg acc ctg tgt cgt ggg gag tat tca atc ctg cat cgc Phe Thr Tyr Arg Thr Leu Cys Arg Gly Glu Tyr Ser Ile Leu His Arg 705 710 715 720	2160
ctt aaa gca gcc atg ggg aca gca tgg cgg gac tat att tcc atc tgc Leu Lys Ala Ala Met Gly Thr Ala Trp Arg Asp Tyr Ile Ser Ile Cys 725 730 735	2208
ggg ctt cgt aca cac gga gag ctg ggc ggg cac ccc gtc tgc gag ctc Gly Leu Arg Thr His Gly Glu Leu Gly Gly His Pro Val Ser Glu Leu 740 745 750	2256
atc tac atc cac agc aag gtg ctc atc gca gat gac cgg aca gtc atc Ile Tyr Ile His Ser Lys Val Leu Ile Ala Asp Asp Arg Thr Val Ile 755 760 765	2304
att ggt tct gca aac atc aat gac cgg agc ttg ctg ggg aag cgg gac Ile Gly Ser Ala Asn Ile Asn Asp Arg Ser Leu Leu Gly Lys Arg Asp 770 775 780	2352
agt gag ctg gcc gtg ctg atc gag gac aca gag acg gaa cca tcc ctc Ser Glu Leu Ala Val Leu Ile Glu Asp Thr Glu Thr Glu Pro Ser Leu 785 790 795 800	2400
atg aat ggg gca gag tat cag gcg ggc agg ttt gcc ttg agt ctg cgg Met Asn Gly Ala Glu Tyr Gln Ala Gly Arg Phe Ala Leu Ser Leu Arg 805 810 815	2448
aag cac tgc ttc ggt gtg att ctt gga gca aat acc cgg cca gac ttg Lys His Cys Phe Gly Val Ile Leu Gly Ala Asn Thr Arg Pro Asp Leu 820 825 830	2496
gat ctc cga gac ccc atc tgt gat gac ttc ttc cag ttg tgg caa gac Asp Leu Arg Asp Pro Ile Cys Asp Asp Phe Phe Gln Leu Trp Gln Asp 835 840 845	2544
atg gct gag agc aac gcc aat atc tat gag cag atc ttc cgc tgc ctg Met Ala Glu Ser Asn Ala Asn Ile Tyr Glu Gln Ile Phe Arg Cys Leu 850 855 860	2592
cca tcc aat gcc acg cgt tcc ctg cgg act ctc cgg gag tac gtg gcc Pro Ser Asn Ala Thr Arg Ser Leu Arg Thr Leu Arg Glu Tyr Val Ala 865 870 875 880	2640
gtg gag ccc ttg gcc acg gtc agt ccc ccc ttg gct cgg tct gag ctc Val Glu Pro Leu Ala Thr Val Ser Pro Pro Leu Ala Arg Ser Glu Leu 885 890 895	2688
acc cag gtc cag ggc cac ctg gtc cac ttc ccc ctc aag ttc cta gag Thr Gln Val Gln Gly His Leu Val His Phe Pro Leu Lys Phe Leu Glu 900 905 910	2736
gat gag tct ttg ctg ccc ccg ctg ggt agc aag gag ggc atg atc ccc Asp Glu Ser Leu Leu Pro Pro Leu Gly Ser Lys Glu Gly Met Ile Pro 915 920 925 930	2784

915

920

cta gaa gtg tgg aca tag
Leu Glu Val Trp Thr
930

2802

<210> 4
<211> 933
<212> PRT
<213> Homo sapiens

<400> 4

Met Thr Ala Thr Pro Glu Ser Leu Phe Pro Thr Gly Asp Glu Leu Asp
1 5 10 15

Ser Ser Gln Leu Gln Met Glu Ser Asp Glu Val Asp Thr Leu Lys Glu
20 25 30

Gly Glu Asp Pro Ala Asp Arg Met His Pro Phe Leu Ala Ile Tyr Glu
35 40 45

Leu Gln Ser Leu Lys Val His Pro Leu Val Phe Ala Pro Gly Val Pro
50 55 60

Val Thr Ala Gln Val Val Gly Thr Glu Arg Tyr Thr Ser Gly Ser Lys
65 70 75 80

Val Gly Thr Cys Thr Leu Tyr Ser Val Arg Leu Thr His Gly Asp Phe
85 90 95

Ser Trp Thr Thr Lys Lys Lys Tyr Arg His Phe Gln Glu Leu His Arg
100 105 110

Asp Leu Leu Arg His Lys Val Leu Met Ser Leu Leu Pro Leu Ala Arg
115 120 125

Phe Ala Val Ala Tyr Ser Pro Ala Arg Asp Ala Gly Asn Arg Glu Met
130 135 140

Pro Ser Leu Pro Arg Ala Gly Pro Glu Gly Ser Thr Arg His Ala Ala
145 150 155 160

Ser Lys Gln Lys Tyr Leu Glu Asn Tyr Leu Asn Cys Leu Leu Thr Met
165 170 175

Ser Phe Tyr Arg Asn Tyr His Ala Met Thr Glu Phe Leu Glu Val Ser

180

185

190

Gln Leu Ser Phe Ile Pro Asp Leu Gly Arg Lys Gly Leu Glu Gly Met
 195 200 205

Ile Arg Lys Arg Ser Gly Gly His Arg Val Pro Gly Leu Thr Cys Cys
 210 215 220

Gly Arg Asp Gln Val Cys Tyr Arg Trp Ser Lys Arg Trp Leu Val Val
 225 230 235 240

Lys Asp Ser Phe Leu Leu Tyr Met Cys Leu Glu Thr Gly Ala Ile Ser
 245 250 255

Phe Val Gln Leu Phe Asp Pro Gly Phe Glu Val Gln Val Gly Lys Arg
 260 265 270

Ser Thr Glu Ala Arg His Gly Val Arg Ile Asp Thr Ser His Arg Ser
 275 280 285

Leu Ile Leu Lys Cys Ser Ser Tyr Arg Gln Ala Arg Trp Trp Ala Gln
 290 295 300

Glu Ile Thr Glu Leu Ala Gln Gly Pro Gly Arg Asp Phe Leu Gln Leu
 305 310 315 320

His Arg His Asp Ser Tyr Ala Pro Pro Arg Pro Gly Thr Leu Ala Arg
 325 330 335

Trp Phe Val Asn Gly Ala Gly Tyr Phe Ala Ala Val Ala Asp Ala Ile
 340 345 350

Leu Arg Ala Gln Glu Glu Ile Phe Ile Thr Asp Trp Trp Leu Ser Pro
 355 360 365

Glu Val Tyr Leu Lys Arg Pro Ala His Ser Asp Asp Trp Arg Leu Asp
 370 375 380

Ile Met Leu Lys Arg Lys Ala Glu Glu Gly Val Arg Val Ser Ile Leu
 385 390 395 400

Leu Phe Lys Glu Val Glu Leu Ala Leu Gly Ile Asn Ser Gly Tyr Ser
 405 410 415

133-PCT1-US1.ST25.txt

Lys Arg Ala Leu Met Leu Leu His Pro Asn Ile Lys Val Met Arg His
 420 425 430

Pro Asp Gln Val Thr Leu Trp Ala His His Glu Lys Leu Leu Val Val
 435 440 445

Asp Gln Val Val Ala Phe Leu Gly Gly Leu Asp Leu Ala Tyr Gly Arg
 450 455 460

Trp Asp Asp Leu His Tyr Arg Leu Thr Asp Leu Gly Asp Ser Ser Glu
 465 470 475 480

Ser Ala Ala Ser Gln Pro Pro Thr Pro Arg Pro Asp Ser Pro Ala Thr
 485 490 495

Pro Asp Leu Ser His Asn Gln Phe Phe Trp Leu Gly Lys Asp Tyr Ser
 500 505 510

Asn Leu Ile Thr Lys Asp Trp Val Gln Leu Asp Arg Pro Phe Glu Asp
 515 520 525

Phe Ile Asp Arg Glu Thr Thr Pro Arg Met Pro Trp Arg Asp Val Gly
 530 535 540

Val Val Val His Gly Leu Pro Ala Arg Asp Leu Ala Arg His Phe Ile
 545 550 555 560

Gln Arg Trp Asn Phe Thr Lys Thr Thr Lys Ala Lys Tyr Lys Thr Pro
 565 570 575

Ile Tyr Pro Tyr Leu Leu Pro Lys Ser Thr Ser Thr Ala Asn Gln Leu
 580 585 590

Pro Phe Thr Leu Pro Gly Gly Gln Cys Thr Thr Val Gln Val Leu Arg
 595 600 605

Ser Val Asp Arg Trp Ser Ala Gly Thr Leu Glu Asn Ser Ile Leu Asn
 610 615 620

Ala Tyr Leu His Thr Ile Arg Glu Ser Gln His Phe Leu Tyr Ile Glu
 625 630 635 640

Asn Gln Phe Phe Ile Ser Cys Ser Asp Gly Arg Thr Val Leu Asn Lys
 645 650 655

133-PCT1-US1.ST25.txt

Val Gly Asp Glu Ile Val Asp Arg Ile Leu Lys Ala His Lys Gln Gly
660 665 670

Trp Cys Tyr Arg Val Tyr Val Leu Leu Pro Leu Leu Pro Gly Phe Glu
675 680 685

Gly Asp Ile Ser Thr Gly Gly Gly Asn Ser Ile Gln Ala Ile Leu His
690 695 700

Phe Thr Tyr Arg Thr Leu Cys Arg Gly Glu Tyr Ser Ile Leu His Arg
705 710 715 720

Leu Lys Ala Ala Met Gly Thr Ala Trp Arg Asp Tyr Ile Ser Ile Cys
725 730 735

Gly Leu Arg Thr His Gly Glu Leu Gly Gly His Pro Val Ser Glu Leu
740 745 750

Ile Tyr Ile His Ser Lys Val Leu Ile Ala Asp Asp Arg Thr Val Ile
755 760 765

Ile Gly Ser Ala Asn Ile Asn Asp Arg Ser Leu Leu Gly Lys Arg Asp
770 775 780

Ser Glu Leu Ala Val Leu Ile Glu Asp Thr Glu Thr Glu Pro Ser Leu
785 790 795 800

Met Asn Gly Ala Glu Tyr Gln Ala Gly Arg Phe Ala Leu Ser Leu Arg
805 810 815

Lys His Cys Phe Gly Val Ile Leu Gly Ala Asn Thr Arg Pro Asp Leu
820 825 830

Asp Leu Arg Asp Pro Ile Cys Asp Asp Phe Phe Gln Leu Trp Gln Asp
835 840 845

Met Ala Glu Ser Asn Ala Asn Ile Tyr Glu Gln Ile Phe Arg Cys Leu
850 855 860

Pro Ser Asn Ala Thr Arg Ser Leu Arg Thr Leu Arg Glu Tyr Val Ala
865 870 875 880

Val Glu Pro Leu Ala Thr Val Ser Pro Pro Leu Ala Arg Ser Glu Leu
885 890 895

133-PCT1-US1.ST25.txt

Thr Gln Val Gln Gly His Leu Val His Phe Pro Leu Lys Phe Leu Glu
900 905 910

Asp Glu Ser Leu Leu Pro Pro Leu Gly Ser Lys Glu Gly Met Ile Pro
915 920 925

Leu Glu Val Trp Thr
930

<210> 5
<211> 1473
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1473)

<400> 5
atg aag cct aaa ctg atg tac cag gag ctg aag gtg cct gca gag gag 48
Met Lys Pro Lys Leu Met Tyr Gln Glu Leu Lys Val Pro Ala Glu Glu
1 5 10 15
ccc gcc aat gag ctg ccc atg aat gag att gag gcg tgg aag gct gcg 96
Pro Ala Asn Glu Leu Pro Met Asn Glu Ile Glu Ala Trp Lys Ala Ala
20 25 30
gaa aag aaa gcc cgc tgg gtc ctg ctg gtc ctc att ctg gcg gtt gtg 144
Glu Lys Lys Ala Arg Trp Val Leu Leu Val Leu Ile Leu Ala Val Val
35 40 45
ggc ttc gga gcc ctg atg act cag ctg ttt cta tgg gaa tac ggc gac 192
Gly Phe Gly Ala Leu Met Thr Gln Leu Phe Leu Trp Glu Tyr Gly Asp
50 55 60
ttg cat ctc ttt ggg ccc aac cag cgc cca gcc ccc tgc tat gac cct 240
Leu His Leu Phe Gly Pro Asn Gln Arg Pro Ala Pro Cys Tyr Asp Pro
65 70 75 80
tgc gaa gca gtg ctg gtg gaa agc att cct gag ggc ctg gac ttc ccc 288
Cys Glu Ala Val Leu Val Glu Ser Ile Pro Glu Gly Leu Asp Phe Pro
85 90 95
aat gcc tcc acg ggg aac cct tcc acc agc cag gcc tgg ctg ggc ctg 336
Asn Ala Ser Thr Gly Asn Pro Ser Thr Ser Gln Ala Trp Leu Gly Leu
100 105 110
ctc gcc ggt gcg cac agc agc ctg gac atc gcc tcc ttc tac tgg acc 384
Leu Ala Gly Ala His Ser Ser Leu Asp Ile Ala Ser Phe Tyr Trp Thr
115 120 125
ctc acc aac aat gac acc cac acg cag gag ccc tct gcc cag cag ggt 432
Leu Thr Asn Asn Asp Thr His Thr Gln Glu Pro Ser Ala Gln Gln Gly

133-PCT1-US1.ST25.txt

130	135	140	
gag gag gtc ctc cgg cag ctg cag acc ctg gca cca aag ggc gtg aac Glu Glu Val Leu Arg Gln Leu Gln Thr Leu Ala Pro Lys Gly Val Asn 145 150 155 160			480
gtc cgc atc gct gtg agc aag ccc agc ggg ccc cag cca cag gcg gac Val Arg Ile Ala Val Ser Lys Pro Ser Gly Pro Gln Pro Gln Ala Asp 165 170 175			528
ctg cag gct ctg ctg cag agc ggt gcc cag gtc cgc atg gtg gac atg Leu Gln Ala Leu Leu Gln Ser Gly Ala Gln Val Arg Met Val Asp Met 180 185 190			576
cag aag ctg acc cat ggc gtc ctg cat acc aag ttc tgg gtg gtg gac Gln Lys Leu Thr His Gly Val Leu His Thr Lys Phe Trp Val Val Asp 195 200 205			624
cag acc cac ttc tac ctg ggc agt gcc aac atg gac tgg cgt tca ctg Gln Thr His Phe Tyr Leu Gly Ser Ala Asn Met Asp Trp Arg Ser Leu 210 215 220			672
acc cag gtc aag gag ctg ggc gtg gtc atg tac aac tgc agc tgc ctg Thr Gln Val Lys Glu Leu Gly Val Val Met Tyr Asn Cys Ser Cys Leu 225 230 235 240			720
gct cga gac ctg acc aag atc ttt gag gcc tac tgg ttc ctg ggc cag Ala Arg Asp Leu Thr Lys Ile Phe Glu Ala Tyr Trp Phe Leu Gly Gln 245 250 255			768
gca ggc agc tcc atc cca tca act tgg ccc cgg ttc tat gac acc cgc Ala Gly Ser Ser Ile Pro Ser Thr Trp Pro Arg Phe Tyr Asp Thr Arg 260 265 270			816
tac aac caa gag aca cca atg gag atc tgc ctc aat gga acc cct gct Tyr Asn Gln Glu Thr Pro Met Glu Ile Cys Leu Asn Gly Thr Pro Ala 275 280 285			864
ctg gcc tac ctg gcg agt gcg ccc cca ccc ctg tgt cca agt ggc cgc Leu Ala Tyr Leu Ala Ser Ala Pro Pro Pro Leu Cys Pro Ser Gly Arg 290 295 300			912
act cca gac ctg aag gct cta ctc aac gtg gtg gac aat gcc cgg agt Thr Pro Asp Leu Lys Ala Leu Leu Asn Val Val Asp Asn Ala Arg Ser 305 310 315 320			960
ttc atc tac gtc gct gtc atg aac tac ctg ccc act ctg gag ttc tcc Phe Ile Tyr Val Ala Val Met Asn Tyr Leu Pro Thr Leu Glu Phe Ser 325 330 335			1008
cac cct cac agg ttc tgg cct gcc att gac gat ggg ctg cgg cgg gcc His Pro His Arg Phe Trp Pro Ala Ile Asp Asp Gly Leu Arg Arg Ala 340 345 350			1056
acc tac gag cgt ggc gtc aag gtg cgc ctg ctc atc agc tgc tgg gga Thr Tyr Glu Arg Gly Val Lys Val Arg Leu Leu Ile Ser Cys Trp Gly 355 360 365			1104
cac tcg gag cca tcc atg cgg gcc ttc ctg ctc tct ctg gct gcc ctg			1152

133-PCT1-US1.ST25.txt

His Ser Glu Pro Ser Met Arg Ala Phe Leu Leu Ser Leu Ala Ala Leu
 370 375 380
 cgt gac aac cat acc cac tct gac atc cag gtg aaa ctc ttt gtg gtc 1200
 Arg Asp Asn His Thr His Ser Asp Ile Gln Val Lys Leu Phe Val Val
 385 390 395 400
 ccc gcg gat gag gcc cag gct cga atc cca tat gcc cgt gtc aac cac 1248
 Pro Ala Asp Glu Ala Gln Ala Arg Ile Pro Tyr Ala Arg Val Asn His
 405 410 415
 aac aag tac atg gtg act gaa cgc gcc acc tac atc gga acc tcc aac 1296
 Asn Lys Tyr Met Val Thr Glu Arg Ala Thr Tyr Ile Gly Thr Ser Asn
 420 425 430
 tgg tct ggc aac tac ttc acg gag acg gcg ggc acc tcg ctg ctg gtg 1344
 Trp Ser Gly Asn Tyr Phe Thr Glu Thr Ala Gly Thr Ser Leu Leu Val
 435 440 445
 acg cag aat ggg agg ggc ggc ctg cgg agc cag ctg gag gcc att ttc 1392
 Thr Gln Asn Gly Arg Gly Gly Leu Arg Ser Gln Leu Glu Ala Ile Phe
 450 455 460
 ctg agg gac tgg gac tcc cct tac agc cat gac ctt gac acc tca gct 1440
 Leu Arg Asp Trp Asp Ser Pro Tyr Ser His Asp Leu Asp Thr Ser Ala
 465 470 475 480
 gac agc gtg ggc aac gcc tgc cgc ctg ctc tga 1473
 Asp Ser Val Gly Asn Ala Cys Arg Leu Leu
 485 490

<210> 6
 <211> 490
 <212> PRT
 <213> Homo sapiens
 <400> 6

Met Lys Pro Lys Leu Met Tyr Gln Glu Leu Lys Val Pro Ala Glu Glu
1 5 10 15

Pro Ala Asn Glu Leu Pro Met Asn Glu Ile Glu Ala Trp Lys Ala Ala
20 25 30

Glu Lys Lys Ala Arg Trp Val Leu Leu Val Leu Ile Leu Ala Val Val
35 40 45

Gly Phe Gly Ala Leu Met Thr Gln Leu Phe Leu Trp Glu Tyr Gly Asp
50 55 60

Leu His Leu Phe Gly Pro Asn Gln Arg Pro Ala Pro Cys Tyr Asp Pro
65 70 75 80

133-PCT1-US1.ST25.txt

Cys Glu Ala Val Leu Val Glu Ser Ile Pro Glu Gly Leu Asp Phe Pro
 85 90 95

Asn Ala Ser Thr Gly Asn Pro Ser Thr Ser Gln Ala Trp Leu Gly Leu
 100 105 110

Leu Ala Gly Ala His Ser Ser Leu Asp Ile Ala Ser Phe Tyr Trp Thr
 115 120 125

Leu Thr Asn Asn Asp Thr His Thr Gln Glu Pro Ser Ala Gln Gln Gly
 130 135 140

Glu Glu Val Leu Arg Gln Leu Gln Thr Leu Ala Pro Lys Gly Val Asn
 145 150 155 160

Val Arg Ile Ala Val Ser Lys Pro Ser Gly Pro Gln Pro Gln Ala Asp
 165 170 175

Leu Gln Ala Leu Leu Gln Ser Gly Ala Gln Val Arg Met Val Asp Met
 180 185 190

Gln Lys Leu Thr His Gly Val Leu His Thr Lys Phe Trp Val Val Asp
 195 200 205

Gln Thr His Phe Tyr Leu Gly Ser Ala Asn Met Asp Trp Arg Ser Leu
 210 215 220

Thr Gln Val Lys Glu Leu Gly Val Val Met Tyr Asn Cys Ser Cys Leu
 225 230 235 240

Ala Arg Asp Leu Thr Lys Ile Phe Glu Ala Tyr Trp Phe Leu Gly Gln
 245 250 255

Ala Gly Ser Ser Ile Pro Ser Thr Trp Pro Arg Phe Tyr Asp Thr Arg
 260 265 270

Tyr Asn Gln Glu Thr Pro Met Glu Ile Cys Leu Asn Gly Thr Pro Ala
 275 280 285

Leu Ala Tyr Leu Ala Ser Ala Pro Pro Pro Leu Cys Pro Ser Gly Arg
 290 295 300

Thr Pro Asp Leu Lys Ala Leu Leu Asn Val Val Asp Asn Ala Arg Ser
 305 310 315 320

133-PCT1-US1.ST25.txt

Phe Ile Tyr Val Ala Val Met Asn Tyr Leu Pro Thr Leu Glu Phe Ser
325 330 335

His Pro His Arg Phe Trp Pro Ala Ile Asp Asp Gly Leu Arg Arg Ala
340 345 350

Thr Tyr Glu Arg Gly Val Lys Val Arg Leu Leu Ile Ser Cys Trp Gly
355 360 365

His Ser Glu Pro Ser Met Arg Ala Phe Leu Leu Ser Leu Ala Ala Leu
370 375 380

Arg Asp Asn His Thr His Ser Asp Ile Gln Val Lys Leu Phe Val Val
385 390 395 400

Pro Ala Asp Glu Ala Gln Ala Arg Ile Pro Tyr Ala Arg Val Asn His
405 410 415

Asn Lys Tyr Met Val Thr Glu Arg Ala Thr Tyr Ile Gly Thr Ser Asn
420 425 430

Trp Ser Gly Asn Tyr Phe Thr Glu Thr Ala Gly Thr Ser Leu Leu Val
435 440 445

Thr Gln Asn Gly Arg Gly Gly Leu Arg Ser Gln Leu Glu Ala Ile Phe
450 455 460

Leu Arg Asp Trp Asp Ser Pro Tyr Ser His Asp Leu Asp Thr Ser Ala
465 470 475 480

Asp Ser Val Gly Asn Ala Cys Arg Leu Leu
485 490

<210> 7
<211> 1467
<212> DNA
<213> Rattus rattus

<220>
<221> CDS
<222> (1)..(1467)

<400> 7
atg aag cct aaa ctg atg tac cag gag ctg aag gtt cct gtt gag gaa
Met Lys Pro Lys Leu Met Tyr Gln Glu Leu Lys Val Pro Val Glu Glu
1 5 10 15

48

133-PCT1-US1.ST25.txt

cct gcg gga gaa ctg ccc atg aat gaa atc gag gca tgg aag gca gca	96
Pro Ala Gly Glu Leu Pro Met Asn Glu Ile Glu Ala Trp Lys Ala Ala	
20 25 30	
gag aag aaa gcc cgt tgg gtc ctc ctt gtc ctt atc ctg gcg gta gtg	144
Glu Lys Lys Ala Arg Trp Val Leu Leu Val Leu Ile Leu Ala Val Val	
35 40 45	
ggc ttc ggt gcc ctg atg act cag ctg ttt cta tgg gaa tac ggg gac	192
Gly Phe Gly Ala Leu Met Thr Gln Leu Phe Leu Trp Glu Tyr Gly Asp	
50 55 60	
tta cat cta ttt ggc ccg aat cag cac cca gcc ccc tgc tat gac ccc	240
Leu His Leu Phe Gly Pro Asn Gln His Pro Ala Pro Cys Tyr Asp Pro	
65 70 75 80	
tgc gag gcg gtg ctg gtg gag agc att ccc gag ggg ctg gag ttt ccc	288
Cys Glu Ala Val Leu Val Glu Ser Ile Pro Glu Gly Leu Glu Phe Pro	
85 90 95	
aat gcc acc aca agc aac ccc tcc acc agc cag gcc tgg ttg ggc ctc	336
Asn Ala Thr Thr Ser Asn Pro Ser Thr Ser Gln Ala Trp Leu Gly Leu	
100 105 110	
ctt gcc ggt gct cac agc agc ctg gac atc gcg tcc ttc tac tgg act	384
Leu Ala Gly Ala His Ser Ser Leu Asp Ile Ala Ser Phe Tyr Trp Thr	
115 120 125	
ctc aca aac aat gat acc cac acg caa gag ccc tct gcc cag cag ggt	432
Leu Thr Asn Asn Asp Thr His Thr Gln Glu Pro Ser Ala Gln Gln Gly	
130 135 140	
gaa gag gtt ctt cag cag ctt cag gct ctg gca cct cga ggt gta aag	480
Glu Glu Val Leu Gln Gln Leu Gln Ala Leu Ala Pro Arg Gly Val Lys	
145 150 155 160	
gtt cgc atc gct gtg agc aaa ccc aac gga cct ctg gct gat ctg cag	528
Val Arg Ile Ala Val Ser Lys Pro Asn Gly Pro Leu Ala Asp Leu Gln	
165 170 175	
tct ctg cta cag agt ggt gcc cag gtg cgc atg gtg gac atg cag aag	576
Ser Leu Leu Gln Ser Gly Ala Gln Val Arg Met Val Asp Met Gln Lys	
180 185 190	
ctg acc cat ggt gtc ctg cac acc aag ttc tgg gtg gtg gac cag acc	624
Leu Thr His Gly Val Leu His Thr Lys Phe Trp Val Val Asp Gln Thr	
195 200 205	
cac ttt tac ctg ggc agt gcc aac atg gac tgg cga tcg ctg acc cag	672
His Phe Tyr Leu Gly Ser Ala Asn Met Asp Trp Arg Ser Leu Thr Gln	
210 215 220	
gtc aag gag ctg ggc gtg gtc atg tac aac tgc agc tgc ctg gct cgc	720
Val Lys Glu Leu Gly Val Val Met Tyr Asn Cys Ser Cys Leu Ala Arg	
225 230 235 240	
gac ctc acc aag att ttt gaa gcc tat tgg ttc ctg ggc cag gca ggc	768
Asp Leu Thr Lys Ile Phe Glu Ala Tyr Trp Phe Leu Gly Gln Ala Gly	

133-PCT1-US1.ST25.txt

245										250										255										
agc	tcc	atc	cct	tca	acc	tgg	cca	cgg	ccc	ttt	gac	acc	cgg	tac	aac		816													
Ser	Ser	Ile	Pro	Ser	Thr	Trp	Pro	Arg	Pro	Phe	Asp	Thr	Arg	Tyr	Asn															
			260					265					270																	
caa	gaa	aca	ccg	atg	gag	atc	tgc	ctc	aat	ggc	acc	cca	gcc	ctg	gcc		864													
Gln	Glu	Thr	Pro	Met	Glu	Ile	Cys	Leu	Asn	Gly	Thr	Pro	Ala	Leu	Ala															
			275				280						285																	
tac	ctg	gcg	agt	gca	ccc	ccg	cca	ctg	tgt	cca	ggg	ggc	cgc	acc	cca		912													
Tyr	Leu	Ala	Ser	Ala	Pro	Pro	Pro	Leu	Cys	Pro	Gly	Gly	Arg	Thr	Pro															
	290					295					300																			
gac	ctg	aag	gca	ctg	ctc	agc	gtg	gtg	gac	aac	gcc	cga	agc	ttc	atc		960													
Asp	Leu	Lys	Ala	Leu	Leu	Ser	Val	Val	Asp	Asn	Ala	Arg	Ser	Phe	Ile															
	305				310					315					320															
tac	att	gca	gtt	atg	aac	tac	ctg	ccc	acc	atg	gag	ttc	tcc	cat	cca		1008													
Tyr	Ile	Ala	Val	Met	Asn	Tyr	Leu	Pro	Thr	Met	Glu	Phe	Ser	His	Pro															
				325					330					335																
cgc	agg	ttc	tgg	cca	gcg	att	gat	gat	ggg	cta	aga	cgg	gct	gcg	tat		1056													
Arg	Arg	Phe	Trp	Pro	Ala	Ile	Asp	Asp	Gly	Leu	Arg	Arg	Ala	Ala	Tyr															
			340				345						350																	
gaa	cga	ggc	gtc	aaa	gtg	cgt	ttg	ctc	atc	agc	tgc	tgg	gga	cac	tcc		1104													
Glu	Arg	Gly	Val	Lys	Val	Arg	Leu	Leu	Ile	Ser	Cys	Trp	Gly	His	Ser															
		355					360					365																		
gag	cca	tcc	atg	cgg	tcc	ttc	ctg	ctc	tcc	ctg	gct	gcc	ctt	cgt	gac		1152													
Glu	Pro	Ser	Met	Arg	Ser	Phe	Leu	Leu	Ser	Leu	Ala	Ala	Leu	Arg	Asp															
	370					375					380																			
aac	cat	acc	cac	tct	gac	atc	cag	gtg	aaa	ctg	ttt	gtg	gtc	cct	gcg		1200													
Asn	His	Thr	His	Ser	Asp	Ile	Gln	Val	Lys	Leu	Phe	Val	Val	Pro	Ala															
	385				390				395						400															
gat	gag	gcc	caa	gct	cga	atc	ccc	tat	gcc	cgc	gtc	aac	cac	aac	aag		1248													
Asp	Glu	Ala	Gln	Ala	Arg	Ile	Pro	Tyr	Ala	Arg	Val	Asn	His	Asn	Lys															
			405					410					415																	
tac	atg	gtg	act	gaa	cgc	acc	aca	tac	att	gga	acc	tcc	aac	tgg	tct		1296													
Tyr	Met	Val	Thr	Glu	Arg	Thr	Thr	Tyr	Ile	Gly	Thr	Ser	Asn	Trp	Ser															
			420					425					430																	
gga	agc	tac	ttc	aca	gag	acg	gca	ggc	acc	tcc	ctg	ctg	gtg	aca	cag		1344													
Gly	Ser	Tyr	Phe	Thr	Glu	Thr	Ala	Gly	Thr	Ser	Leu	Leu	Val	Thr	Gln															
		435					440					445																		
aac	ggg	cac	ggg	ggc	ttg	cgc	agc	cag	ctg	gag	gct	gtt	ttc	ctg	aga		1392													
Asn	Gly	His	Gly	Gly	Leu	Arg	Ser	Gln	Leu	Glu	Ala	Val	Phe	Leu	Arg															
	450					455					460																			
gac	tgg	gaa	tcc	cca	tac	agc	cac	aac	ctt	gac	acc	tca	gcc	gac	agt		1440													
Asp	Trp	Glu	Ser	Pro	Tyr	Ser	His	Asn	Leu	Asp	Thr	Ser	Ala	Asp	Ser															
	465				470					475					480															
gtg	ggc	aat	gcc	tgc	cgc	ctg	ctt	tga									1467													

133-PCT1-US1.ST25.txt

Val Gly Asn Ala Cys Arg Leu Leu
485

<210> 8
<211> 488
<212> PRT
<213> Rattus rattus

<400> 8

Met Lys Pro Lys Leu Met Tyr Gln Glu Leu Lys Val Pro Val Glu Glu
1 5 10 15

Pro Ala Gly Glu Leu Pro Met Asn Glu Ile Glu Ala Trp Lys Ala Ala
20 25 30

Glu Lys Lys Ala Arg Trp Val Leu Leu Val Leu Ile Leu Ala Val Val
35 40 45

Gly Phe Gly Ala Leu Met Thr Gln Leu Phe Leu Trp Glu Tyr Gly Asp
50 55 60

Leu His Leu Phe Gly Pro Asn Gln His Pro Ala Pro Cys Tyr Asp Pro
65 70 75 80

Cys Glu Ala Val Leu Val Glu Ser Ile Pro Glu Gly Leu Glu Phe Pro
85 90 95

Asn Ala Thr Thr Ser Asn Pro Ser Thr Ser Gln Ala Trp Leu Gly Leu
100 105 110

Leu Ala Gly Ala His Ser Ser Leu Asp Ile Ala Ser Phe Tyr Trp Thr
115 120 125

Leu Thr Asn Asn Asp Thr His Thr Gln Glu Pro Ser Ala Gln Gln Gly
130 135 140

Glu Glu Val Leu Gln Gln Leu Gln Ala Leu Ala Pro Arg Gly Val Lys
145 150 155 160

Val Arg Ile Ala Val Ser Lys Pro Asn Gly Pro Leu Ala Asp Leu Gln
165 170 175

Ser Leu Leu Gln Ser Gly Ala Gln Val Arg Met Val Asp Met Gln Lys
180 185 190

133-PCT1-US1.ST25.txt

Leu Thr His Gly Val Leu His Thr Lys Phe Trp Val Val Asp Gln Thr
 195 200 205

His Phe Tyr Leu Gly Ser Ala Asn Met Asp Trp Arg Ser Leu Thr Gln
 210 215 220

Val Lys Glu Leu Gly Val Val Met Tyr Asn Cys Ser Cys Leu Ala Arg
 225 230 235 240

Asp Leu Thr Lys Ile Phe Glu Ala Tyr Trp Phe Leu Gly Gln Ala Gly
 245 250 255

Ser Ser Ile Pro Ser Thr Trp Pro Arg Pro Phe Asp Thr Arg Tyr Asn
 260 265 270

Gln Glu Thr Pro Met Glu Ile Cys Leu Asn Gly Thr Pro Ala Leu Ala
 275 280 285

Tyr Leu Ala Ser Ala Pro Pro Pro Leu Cys Pro Gly Gly Arg Thr Pro
 290 295 300

Asp Leu Lys Ala Leu Leu Ser Val Val Asp Asn Ala Arg Ser Phe Ile
 305 310 315 320

Tyr Ile Ala Val Met Asn Tyr Leu Pro Thr Met Glu Phe Ser His Pro
 325 330 335

Arg Arg Phe Trp Pro Ala Ile Asp Asp Gly Leu Arg Arg Ala Ala Tyr
 340 345 350

Glu Arg Gly Val Lys Val Arg Leu Leu Ile Ser Cys Trp Gly His Ser
 355 360 365

Glu Pro Ser Met Arg Ser Phe Leu Leu Ser Leu Ala Ala Leu Arg Asp
 370 375 380

Asn His Thr His Ser Asp Ile Gln Val Lys Leu Phe Val Val Pro Ala
 385 390 395 400

Asp Glu Ala Gln Ala Arg Ile Pro Tyr Ala Arg Val Asn His Asn Lys
 405 410 415

Tyr Met Val Thr Glu Arg Thr Thr Tyr Ile Gly Thr Ser Asn Trp Ser
 420 425 430

133-PCT1-US1.ST25.txt

Gly Ser Tyr Phe Thr Glu Thr Ala Gly Thr Ser Leu Leu Val Thr Gln
 435 440 445

Asn Gly His Gly Gly Leu Arg Ser Gln Leu Glu Ala Val Phe Leu Arg
 450 455 460

Asp Trp Glu Ser Pro Tyr Ser His Asn Leu Asp Thr Ser Ala Asp Ser
 465 470 475 480

Val Gly Asn Ala Cys Arg Leu Leu
 485